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<p><b>(54) Title:</b> GENETIC ANALYSIS</p> <p><b>(57) Abstract</b></p> <p>A method is described for use in whole genome analysis. The method – termed inter-population perfectly matched duplex depletion – can overcome many of the limitations of current approaches based upon SNPs and linkage disequilibrium within isolated populations. Inter-population perfectly matched duplex depletion isolates a fragment (or fragments) containing differences between the "affected" and "unaffected" populations or cells. A convenient method – terminal restriction site profiling arrays (TRSPAs) – is described for the analysis of such fragments. A totally diagnostic internal control DNA is also described which allows both the extent and exact nature of any partial digestion to be unambiguously determined for inter-population perfectly matched duplex depletion or TRSPA restriction.</p>			

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